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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/908,988B

DATE: 02/26/2002

TIME: 14:06:37

Input Set : A:\MYOG028.txt

Output Set: N:\CRF3\02262002\I908988B.raw

3 <110> APPLICANT: OLSON, ERIC  
4 SPENCER, JEFFREY A.  
6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES  
7 IN STRIATED MUSCLE CELLS  
9 <130> FILE REFERENCE: MYOG:028US  
11 <140> CURRENT APPLICATION NUMBER: 09/908,988B  
C--> 12 <141> CURRENT FILING DATE: 2000-07-18  
14 <150> PRIOR APPLICATION NUMBER: 60/219,020  
15 <151> PRIOR FILING DATE: 2000-07-18  
17 <160> NUMBER OF SEQ ID NOS: 6  
19 <170> SOFTWARE: PatentIn Ver. 2.1  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 1431  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Mus musculus  
26 <220> FEATURE:  
27 <221> NAME/KEY: CDS  
28 <222> LOCATION: (199)..(1296)  
30 <400> SEQUENCE: 1  
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33 gacaggactc ttccaaaggagg gagcaatagc cgggatccca agaatccagt cagcctaaac 120  
35 tgaccgagga agggtgcaca ggcaggggag aaggccaacg acaggccac agcgaggcag 180  
37 gctccagagc gccgcggg atg aac ttc acg gtg ggt ttc aag ccg ctg cta 231  
38 Met Asn Phe Thr Val Gly Phe Lys Pro Leu Leu  
39 1 5 10  
41 ggg gat gcg cac aac atg gac aac ttg gag aag cag ctc att tgc ccc 279  
42 Gly Asp Ala His Asn Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro  
43 15 20 25  
45 atc tgc ctg gag atg ttc tcc aag ccc gtg gtg atc ttg ccc tgc caa 327  
46 Ile Cys Leu Glu Met Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln  
47 30 35 40  
49 cac aac ctg tgc cgc aag tgt gcc aac gac gtc ttc cag gcc tct aat 375  
50 His Asn Leu Cys Arg Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn  
51 45 50 55  
53 cct ctg tgg caa tcc cgg ggc tcc aca acg gtg tct tca gga gga cgt 423  
54 Pro Leu Trp Gln Ser Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg  
55 60 65 70 75  
57 ttc cga tgc cca tct tgt agg cac gag gtt gtc ctg gac agg cat ggt 471  
58 Phe Arg Cys Pro Ser Cys Arg His Glu Val Val Leu Asp Arg His Gly  
59 80 85 90  
61 gtc tat ggc ctg cag cgg aac ctg cta gtg gag aac atc att gac atc 519  
62 Val Tyr Gly Leu Gln Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile  
63 95 100 105

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|   |      |
|---|------|
| 65 tac aag cag gag tcc tcc cgg cca ctg cac gcc aag gct gaa cag cac  | 567  |
| 66 Tyr Lys Gln Glu Ser Ser Arg Pro Leu His Ala Lys Ala Glu Gln His  |      |
| 67 110 115 120  |      |
| 69 ctc atg tgt gag gag cac gag gac gag aag atc aac atc tac tgc ctg  | 615  |
| 70 Leu Met Cys Glu His Glu Asp Glu Lys Ile Asn Ile Tyr Cys Leu      |      |
| 71 125 130 135  |      |
| 73 agc tgc gag gtg ccc acc tgc tct ctc tgc aag gtt ttc ggc gcc cac  | 663  |
| 74 Ser Cys Glu Val Pro Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His  |      |
| 75 140 145 150 155  |      |
| 77 aag gac tgt gag gtg gcc cct ctg ccc acc att tac aaa cgc cag aag  | 711  |
| 78 Lys Asp Cys Glu Val Ala Pro Leu Pro Thr Ile Tyr Lys Arg Gln Lys  |      |
| 79 160 165 170  |      |
| 81 agt gag ctg agc gat ggc atc gcg atg ctg gtg gcg ggc aat gac cgt  | 759  |
| 82 Ser Glu Leu Ser Asp Gly Ile Ala Met Leu Val Ala Gly Asn Asp Arg  |      |
| 83 175 180 185  |      |
| 85 gtg cag gca gtg atc acc cag atg gag gag gtg tgc cag acc att gag  | 807  |
| 86 Val Gln Ala Val Ile Thr Gln Met Glu Glu Val Cys Gln Thr Ile Glu  |      |
| 87 190 195 200  |      |
| 89 gac aac agc cgc aga cag aag caa ctg tta aac cag agg ttc gag acc  | 855  |
| 90 Asp Asn Ser Arg Arg Gln Lys Gln Leu Leu Asn Gln Arg Phe Glu Thr  |      |
| 91 205 210 215  |      |
| 93 ctg tgc gcg gtt ttg gag gag cgc aag ggc gaa ctg ctt caa gca ctg  | 903  |
| 94 Leu Cys Ala Val Leu Glu Glu Arg Lys Gly Glu Leu Leu Gln Ala Leu  |      |
| 95 220 225 230 235  |      |
| 97 gcc cgg gag cag gag aag ttg cag cgc gtg cgg ggc ctc atc cgc      | 951  |
| 98 Ala Arg Glu Gln Glu Glu Lys Leu Gln Arg Val Arg Gly Leu Ile Arg  |      |
| 99 240 245 250  |      |
| 101 cag tac gga gac cac ttg gag ggc tcc tca aag ctg gtg gag tcc gcc | 999  |
| 102 Gln Tyr Gly Asp His Leu Glu Gly Ser Ser Lys Leu Val Glu Ser Ala |      |
| 103 255 260 265   |      |
| 105 atc cag tcc atg gag gag ccg cag atg gct ctc tac ctc cag cag gca | 1047 |
| 106 Ile Gln Ser Met Glu Glu Pro Gln Met Ala Leu Tyr Leu Gln Gln Ala |      |
| 107 270 275 280   |      |
| 109 aag gag ctg atc aac aag gtc ggg gca atg tcg aag gtg gag ctg gca | 1095 |
| 110 Lys Glu Leu Ile Asn Lys Val Gly Ala Met Ser Lys Val Glu Leu Ala |      |
| 111 285 290 295   |      |
| 113 gga cgg ccg gag cca ggc tat gag agc atg gag caa ttc tct gtg agc | 1143 |
| 114 Gly Arg Pro Glu Pro Gly Tyr Glu Ser Met Glu Gln Phe Ser Val Ser |      |
| 115 300 305 310 315   |      |
| 117 gtg gag cac gtg gcc gaa atg ttg cga acc atc gac ttc cag ccg ggc | 1191 |
| 118 Val Glu His Val Ala Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly |      |
| 119 320 325 330   |      |
| 121 gcc gct ggg gat gaa gag gat gac gac atg gct ttg gat ggg gag gag | 1239 |
| 122 Ala Ala Gly Asp Glu Glu Asp Asp Met Ala Leu Asp Gly Glu Glu     |      |
| 123 335 340 345   |      |
| 125 ggc aat gcg ggg ctg gag gag cgg ctg gac gtg cca gaa ggc tca     | 1287 |
| 126 Gly Asn Ala Gly Leu Glu Glu Arg Leu Asp Val Pro Glu Gly Ser     |      |
| 127 350 355 360   |      |
| 129 ggc ctg cac tgacccgact ctgatccaga gcgcacaccc gaagcgaggag        | 1336 |

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130 Gly Leu His  
131 365  
133 ccaaggatg ctgaggatct gcgcagagac caccgcgcca ccaagctcggttccggccc 1396  
135 cccggaaagggt tctcaataaa ggactcaagt gtccc 1431  
138 <210> SEQ ID NO: 2  
139 <211> LENGTH: 366  
140 <212> TYPE: PRT  
141 <213> ORGANISM: Mus musculus  
143 <400> SEQUENCE: 2  
144 Met Asn Phe Thr Val Gly Phe Lys Pro Leu Leu Gly Asp Ala His Asn  
145 1 5 10 15  
147 Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met  
148 20 25 30  
150 Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg  
151 35 40 45  
153 Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn Pro Leu Trp Gln Ser  
154 50 55 60  
156 Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg Phe Arg Cys Pro Ser  
157 65 70 75 80  
159 Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu Gln  
160 85 90 95  
162 Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Ser  
163 100 105 110  
165 Ser Arg Pro Leu His Ala Lys Ala Glu Gln His Leu Met Cys Glu Glu  
166 115 120 125  
168 His Glu Asp Glu Lys Ile Asn Ile Tyr Cys Leu Ser Cys Glu Val Pro  
169 130 135 140  
171 Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp Cys Glu Val  
172 145 150 155 160  
174 Ala Pro Leu Pro Thr Ile Tyr Lys Arg Gln Lys Ser Glu Leu Ser Asp  
175 165 170 175  
177 Gly Ile Ala Met Leu Val Ala Gly Asn Asp Arg Val Gln Ala Val Ile  
178 180 185 190  
180 Thr Gln Met Glu Glu Val Cys Gln Thr Ile Glu Asp Asn Ser Arg Arg  
181 195 200 205  
183 Gln Lys Gln Leu Leu Asn Gln Arg Phe Glu Thr Leu Cys Ala Val Leu  
184 210 215 220  
186 Glu Glu Arg Lys Gly Glu Leu Leu Gln Ala Leu Ala Arg Glu Gln Glu  
187 225 230 235 240  
189 Glu Lys Leu Gln Arg Val Arg Gly Leu Ile Arg Gln Tyr Gly Asp His  
190 245 250 255  
192 Leu Glu Gly Ser Ser Lys Leu Val Glu Ser Ala Ile Gln Ser Met Glu  
193 260 265 270  
195 Glu Pro Gln Met Ala Leu Tyr Leu Gln Ala Lys Glu Leu Ile Asn  
196 275 280 285  
198 Lys Val Gly Ala Met Ser Lys Val Glu Leu Ala Gly Arg Pro Glu Pro  
199 290 295 300  
201 Gly Tyr Glu Ser Met Glu Gln Phe Ser Val Ser Val Glu His Val Ala  
202 305 310 315 320

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204 Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly Ala Ala Gly Asp Glu  
 205 325 330 335  
 207 Glu Asp Asp Asp Met Ala Leu Asp Gly Glu Glu Gly Asn Ala Gly Leu  
 208 340 345 350  
 210 Glu Glu Glu Arg Leu Asp Val Pro Glu Gly Ser Gly Leu His  
 211 355 360 365  
 215 <210> SEQ ID NO: 3  
 216 <211> LENGTH: 2590  
 217 <212> TYPE: DNA  
 218 <213> ORGANISM: Mus musculus  
 220 <220> FEATURE:  
 221 <221> NAME/KEY: CDS  
 222 <222> LOCATION: (80)..(1714)  
 224 <400> SEQUENCE: 3  
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 227 ggacagggac ggcaaggaa atg agc act tct ctg aat tac aag tct ttc tcc 112  
 228 Met Ser Thr Ser Leu Asn Tyr Lys Ser Phe Ser  
 229 1 5 10  
 231 aaa gag cag cag acc atg gat aac ttg gaa aag caa ctg atc tgt ccc 160  
 232 Lys Glu Gln Gln Thr Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro  
 233 15 20 25  
 235 atc tgc cta gag atg ttc acg aag cct gtg gtc att ctc cct tgc cag 208  
 236 Ile Cys Leu Glu Met Phe Thr Lys Pro Val Val Ile Leu Pro Cys Gln  
 237 30 35 40  
 239 cac aac ctg tgc agg aaa tgt gcc agt gac atc ttc cag gcc tct aac 256  
 240 His Asn Leu Cys Arg Lys Cys Ala Ser Asp Ile Phe Gln Ala Ser Asn  
 241 45 50 55  
 243 ccg tac tta ccc aca aga gga ggc acc acc gtg gca tca ggg ggc cgc 304  
 244 Pro Tyr Leu Pro Thr Arg Gly Gly Thr Thr Val Ala Ser Gly Gly Arg  
 245 60 65 70 75  
 247 ttc cgc tgt ccc tcc tgc aga cat gag gtg gtg tta gac aga cat ggg 352  
 248 Phe Arg Cys Pro Ser Cys Arg His Glu Val Val Leu Asp Arg His Gly  
 249 80 85 90  
 251 gtc tat gga ctg cag agg aac ctg ctc gtg gaa aac att att gat atc 400  
 252 Val Tyr Gly Leu Gln Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile  
 253 95 100 105  
 255 tac aag cag gaa tcc acc agg cca gaa aaa aaa ttg gac cag ccc atg 448  
 256 Tyr Lys Gln Glu Ser Thr Arg Pro Glu Lys Lys Leu Asp Gln Pro Met  
 257 110 115 120  
 259 tgt gaa gag cat gaa gag gaa cgc atc aac atc tat tgt ctg aac tgt 496  
 260 Cys Glu Glu His Glu Glu Arg Ile Asn Ile Tyr Cys Leu Asn Cys  
 261 125 130 135  
 263 gaa gtg ccc acc tgt tcc ttg tgc aag gtt ttt ggc gcc cat aag gac 544  
 264 Glu Val Pro Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp  
 265 140 145 150 155  
 267 tgc cag gtg gct ccc ctg act cat gtg ttc cag agg cag aag tca gag 592  
 268 Cys Gln Val Ala Pro Leu Thr His Val Phe Gln Arg Gln Lys Ser Glu  
 269 160 165 170  
 271 ctc agt gat ggt att gct ctt gtg gga agc aac gat aga gtc cag 640

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|     |   |      |     |     |
|-----|---|------|-----|-----|
| 272 | Leu Ser Asp Gly Ile Ala Val Leu Val Gly Ser Asn Asp Arg Val Gln |      |     |     |
| 273 | 175   | 180  | 185 |     |
| 275 | ggt gtg atc agc cag ctg gag gac acc tgt aaa act att gag gag tgc | 688  |     |     |
| 276 | Gly Val Ile Ser Gln Leu Glu Asp Thr Cys Lys Thr Ile Glu Glu Cys |      |     |     |
| 277 | 190   | 195  | 200 |     |
| 279 | tgc aga aag cag aaa cag gac ctg tgt gag aaa ttt gat cac cta tac | 736  |     |     |
| 280 | Cys Arg Lys Gln Lys Gln Asp Leu Cys Glu Lys Phe Asp His Leu Tyr |      |     |     |
| 281 | 205   | 210  | 215 |     |
| 283 | ggc atc ctg gag gag agg aag act gaa atg acc caa gcc atc act cga | 784  |     |     |
| 284 | Gly Ile Leu Glu Glu Arg Lys Thr Glu Met Thr Gln Ala Ile Thr Arg |      |     |     |
| 285 | 220   | 225  | 230 | 235 |
| 287 | aca cag gag gag aaa ctg gaa cat gtc cga act ctt atc agg aag tat | 832  |     |     |
| 288 | Thr Gln Glu Glu Lys Leu Glu His Val Arg Thr Leu Ile Arg Lys Tyr |      |     |     |
| 289 | 240   | 245  | 250 |     |
| 291 | tcc gat cac ctg gag aac gta tcc aag ttg gtg gag tca gga atc cag | 880  |     |     |
| 292 | Ser Asp His Leu Glu Asn Val Ser Lys Leu Val Glu Ser Gly Ile Gln |      |     |     |
| 293 | 255   | 260  | 265 |     |
| 295 | ttc atg gat gag ccc gaa atg gca gta ttt ctg cag aat gcc aag acc | 928  |     |     |
| 296 | Phe Met Asp Glu Pro Glu Met Ala Val Phe Leu Gln Asn Ala Lys Thr |      |     |     |
| 297 | 270   | 275  | 280 |     |
| 299 | ctg ttg caa aag atc gtg gaa gca tca aag gcg ttt cag atg gag aaa | 976  |     |     |
| 300 | Leu Leu Gln Lys Ile Val Glu Ala Ser Lys Ala Phe Gln Met Glu Lys |      |     |     |
| 301 | 285   | 290  | 295 |     |
| 303 | cta gaa caa ggt tat gag atc atg agc aac ttc act gtc aat ctc aat | 1024 |     |     |
| 304 | Leu Glu Gln Gly Tyr Glu Ile Met Ser Asn Phe Thr Val Asn Leu Asn |      |     |     |
| 305 | 300   | 305  | 310 | 315 |
| 307 | aga gaa gaa aaa att atc cgt gaa att gac ttt tct aga gaa gag gaa | 1072 |     |     |
| 308 | Arg Glu Glu Lys Ile Ile Arg Glu Ile Asp Phe Ser Arg Glu Glu Glu |      |     |     |
| 309 | 320   | 325  | 330 |     |
| 311 | gag gaa gaa gat gca gga gaa ata gat gaa gaa gga gaa gga gag gat | 1120 |     |     |
| 312 | Glu Glu Glu Asp Ala Gly Glu Ile Asp Glu Glu Gly Glu Gly Glu Asp |      |     |     |
| 313 | 335   | 340  | 345 |     |
| 315 | gca gta gaa gta gaa gag gca gaa aat gtt caa ata gca tct tca ggg | 1168 |     |     |
| 316 | Ala Val Glu Val Glu Ala Glu Asn Val Gln Ile Ala Ser Ser Gly     |      |     |     |
| 317 | 350   | 355  | 360 |     |
| 319 | gaa gag gag agt ctg gag aaa gct gca gag ccc tct cag ctt ccc gca | 1216 |     |     |
| 320 | Glu Glu Glu Ser Leu Glu Lys Ala Ala Glu Pro Ser Gln Leu Pro Ala |      |     |     |
| 321 | 365   | 370  | 375 |     |
| 323 | gag ctt cag gtc gcc cca gag cca cta cct gct tcc tct cca gaa ccg | 1264 |     |     |
| 324 | Glu Leu Gln Val Ala Pro Glu Pro Leu Pro Ala Ser Ser Pro Glu Pro |      |     |     |
| 325 | 380   | 385  | 390 | 395 |
| 327 | ttt tca tcc atg cca cct gct gca gat gtc ctg gtg aca cag ggg gag | 1312 |     |     |
| 328 | Phe Ser Ser Met Pro Pro Ala Ala Asp Val Leu Val Thr Gln Gly Glu |      |     |     |
| 329 | 400   | 405  | 410 |     |
| 331 | gtg gtg ccc att ggc tct cag cag acc aca cag tct gaa act tca ggc | 1360 |     |     |
| 332 | Val Val Pro Ile Gly Ser Gln Gln Thr Thr Gln Ser Glu Thr Ser Gly |      |     |     |
| 333 | 415   | 420  | 425 |     |
| 335 | cct tca gca gcg gaa act gcg gat ccc ttg ttt tac cct agt tgg tat | 1408 |     |     |
| 336 | Pro Ser Ala Ala Glu Thr Ala Asp Pro Leu Phe Tyr Pro Ser Trp Tyr |      |     |     |

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